

Application No.: 10/718952
Docket No.: BB1077USDIV

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REMARKS

Claims 1,3,4,6,7,9 and 10 are currently pending in the application.

Claims 1 and 7 have been amended and the term "using" has been replaced with the term "based on". Support for this change is found throughout the specification as filed, for example on page 10 at lines 17-31. It is believed that no new matter has been added.

The text added to claim 7 "or 11 based on the Clustal method of alignment" has been underlined and is now in compliance with Rule 1.121 which requires that the text of any added subject matter to be shown by underlining. No new matter has been added.

Claim 4 has been amended for purposes of clarification. It is believed that no new matter has been added.

Claims 1 and 7 were rejected under 35 U.S.C. § 112 , first paragraph, as being indefinite for failing to particular point out and distinctly claim the subject matter which applicant regards as the invention. The term "the Clustal method of alignment" refers to the Clustal method of alignment described in the specification on page 10 at lines 24-30. Withdrawal of this ground of rejection of claims 1 and 7 is respectfully requested in view of the above discussion and amendments.

Claims 1 and 6-7 were rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the enablement requirement, on the ground that the specification does not reasonably provide enablement for all nucleic acid fragments encoding a soybean myo-inositol phosphate synthase (MIPS) including those that have 90% sequence identity to SEQ ID NO: 1,5,11 or 15 and the complement or subfragment thereof.

Enclosed herewith is Appendix A sets forth a comparison of the nucleic acid sequences of wild type and mutant soybean *myo*-inositol 1-phosphate synthases.

This alignment also identifies the conserved nucleic acid sequence motifs corresponding to the amino acid sequence motifs disclosed by Majumder et al. (2003, FEBS Lett. 553: 3-10) and Majumder et al (1997, Biochim. Biophys. Acta 1348: 245-256):

a) the GXGGXG motif is set forth as GWGGNNG in the sequences of the invention and corresponds to the underlined nucleic acid sequence designated Motif I;

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- b) the "LWTANTERY" motif corresponds to the underlined nucleic acid sequence designated Motif II;
- c) the "NGSPQNTFVPGL" motif corresponds to the underlined nucleic acid sequence designated Motif III; and
- d) the "SYNHLGNNDG" motif corresponds to the underlined nucleic acid sequence designated Motif IV.

All of these motifs are conserved at the nucleic acid level among the sequences of the invention. Altogether, 114 nucleic acid residues are encompassed.

Furthermore, the instant specification also discloses the following:

a) two allelic wild-type soybean MIPS nucleic acid sequences (SEQ ID NO: 1 and 15 that vary in 42 nucleic acid residues as indicated by an open arrow in the alignment set forth in Appendix A. Since SEQ ID NOs 1 and 15 correspond to wild type MIPS, it appears that these variations in the nucleic acid sequence do not affect functionality of the enzyme; and

b) two mutant soybean MIPS nucleic sequences as set forth in SEQ ID NOs: 5 and 11 that have 2 nucleotide changes. These changes are indicated by a darkened triangle appearing over the mutated residues. These mutated residues appear to be important for functionality of the enzyme.

Thus, 158 nucleic acid residues, out of the approximately 1500 coding for a soybean MIPS, have been described in terms of importance to maintain or alter function of a MIPS enzyme. Therefore, it is believed that sufficient guidance has been provided to one of ordinary skill in the art as to which soybean nucleic acid fragments within 90% sequence identity, subfragments and complements thereof constitute a part of the invention. One of ordinary skill in the art would be able to practice the instant invention without engaging in undue experimentation to screen through a vast number of soybean clones to identify those having 90% sequence identity with the claimed sequences encoding either a wild type MIPS or a mutant MIPS.

Accordingly, withdrawal of the rejection of the claims under 35 U.S.C. § 112, first paragraph, as lacking enablement is respectfully requested.

A petition for an Extension of Time for One (1) month accompanies this response along with Appendix A and a Notice of Appeal.

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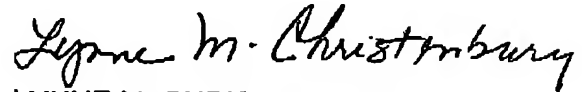
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It is respectfully submitted that the claims are now in form for allowance which allowance is respectfully requested.

Please credit any overpayment and charge any fees which are required in connection with the filing of the response to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

Respectfully submitted,



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Dated: August 15, 2006

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APPENDIX A

Appendix A shows a comparison of the nucleic acid sequences of wild type and mutant soybean *myo*-inositol 1-phosphate synthases. Dashes are used by the program to maximize alignment of the sequences. The conserved nucleic acid sequences (motifs I, II, III and IV) corresponding to the amino acid sequence motifs disclosed by Majumder et al. (2003, FEBS Lett. 553: 3-10) and Majumder et al (1997, Biochim. Biophys. Acta 1348: 245-256) are underlined. Forty-two nucleic acid residue changes in the two allelic wild-type soybean *myo*-inositol 1-phosphate synthases (SEQ ID NO: 1 and 15) are indicated by an open triangle above the alignment. Nucleic acid residue changes in the nucleic acid sequences of mutant lines corresponding to SEQ ID NO: 5 and 11 are indicated by a closed or darkened triangle above the alignment.

```
SEQ ID NO:1  CTCTTCITTTATTTCCTTTTGTAATTTTCATTCTTAATCTTTGTGAAAAATAATGTTCA
SEQ ID NO:5  -----ATGTTCA
SEQ ID NO:9  -----ATGTTCA
SEQ ID NO:11 -----ATGTTCA
SEQ ID NO:13 -----ATGTTCA
SEQ ID NO:15 -----ATGTTCA
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          Δ Δ
SEQ ID NO:1  TCGAGAATTTTAAGGTTGAGTGTCTTAATGTGAAGTACACCGAGACTGAGATTTCAGTCCG
SEQ ID NO:5  TCGAGAATTTTAAGGTTGAGTGTCTTAATGTGAAGTACACCGAGACTGAGATTTCAGTCCG
SEQ ID NO:9  TCGAGAATTTTAAGGTTGAGTGTCTTAATGTGAAGTACACCGAGACTGAGATTTCAGTCCG
SEQ ID NO:11 TCGAGAATTTTAAGGTTGAGTGTCTTAATGTGAAGTACACCGAGACTGAGATTTCAGTCCG
SEQ ID NO:13 TCGAGAATTTTAAGGTTGAGTGTCTTAATGTGAAGTACACCGAGACTGAGATTTCAGTCCG
SEQ ID NO:15 TCGAGAATTTTAAGGTTGAGTGTCTTAATGTGAAGTACACCGAGACTGAGATTTCAGTCCG
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SEQ ID NO:1  TGTACAACCTACGAAACCACCGAACTTGTTCACGAGAACAGGAATGGCACCTATCAGTGGA
SEQ ID NO:5  TGTACAACCTACGAAACCACCGAACTTGTTCACGAGAACAGGAATGGCACCTATCAGTGGA
SEQ ID NO:9  TGTACAACCTACGAAACCACCGAACTTGTTCACGAGAACAGGAATGGCACCTATCAGTGGA
SEQ ID NO:11 TGTACAACCTACGAAACCACCGAACTTGTTCACGAGAACAGGAATGGCACCTATCAGTGGA
SEQ ID NO:13 TGTACAACCTACGAAACCACCGAACTTGTTCACGAGAACAGGAATGGCACCTATCAGTGGA
SEQ ID NO:15 TGTACAACCTACGAAACCACCGAACTTGTTCACGAGAACAGGAATGGCACCTATCAGTGGA
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          Δ Δ Δ Δ Δ Δ Δ
SEQ ID NO:1  TTGTCAAACCCAAATCTGTCAAATACGAATTTAAAACCAACATCCATGTTCCCTAAATTAG
SEQ ID NO:5  TTGTCAAACCCAAATCTGTCAAATACGAATTTAAAACCAACATCCATGTTCCCTAAATTAG
SEQ ID NO:9  TTGTCAAACCCAAATCTGTCAAATACGAATTTAAAACCAACATCCATGTTCCCTAAATTAG
SEQ ID NO:11 TTGTCAAACCCAAATCCGTCAACTACCAATTTAAAACCAACATCCATGTTCCCTAAATTAG
SEQ ID NO:13 TTGTCAAACCCAAATCCGTCAACTACCAATTTAAAACCAACATCCATGTTCCCTAAATTAG
SEQ ID NO:15 TTGTCAAACCCAAATCCGTCAACTACCAATTTAAAACCAACATCCATGTTCCCTAAATTAG
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```
          Δ Δ
SEQ ID NO:1  GGGTAATGCTTGTGGGTTGGGGTGGAAACAACGGCTCAACCCCTACCGGTGGTGTATTG
SEQ ID NO:5  GGGTAATGCTTGTGGGTTGGGGTGGAAACAACGGCTCAACCCCTACCGGTGGTGTATTG
SEQ ID NO:9  GGGTAATGCTTGTGGGTTGGGGTGGAAACAACGGCTCAACCCCTACCGGTGGTGTATTG
SEQ ID NO:11 GGGTGATGCTTGTGGGTTGGGGTGGAAACAACGGCTCTACCCCTACCGGTGGTGTATTG
SEQ ID NO:13 GGGTGATGCTTGTGGGTTGGGGTGGAAACAACGGCTCTACCCCTACCGGTGGTGTATTG
SEQ ID NO:15 GGGTGATGCTTGTGGGTTGGGGTGGAAACAACGGCTCTACCCCTACCGGTGGTGTATTG
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Motif I

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SEQ ID NO:1 CTAACCGAGAGGGCATTTCATGGGCTACAAAGGACAAGATTCAACAAGCCAATTACTTTG
SEQ ID NO:5 CTAACCGAGAGGGCATTTCATGGGCTACAAAGGACAAGATTCAACAAGCCAATTACTTTG
SEQ ID NO:9 CTAACCGAGAGGGCATTTCATGGGCTACAAAGGACAAGATTCAACAAGCCAATTACTTTG
SEQ ID NO:11 CTAACAGAGAGGACATTTCATGGGCTACAAAGGACAAGATTCAACAAGCCAATTACTTTG
SEQ ID NO:13 CTAACAGAGAGGGCATTTCATGGGCTACAAAGGACAAGATTCAACAAGCCAATTACTTTG
SEQ ID NO:15 CTAACAGAGAGGGCATTTCATGGGCTACAAAGGACAAGATTCAACAAGCCAATTACTTTG

SEQ ID NO:1 GCTCCCTCACCCAAGCCTCAGCTATCCGAGTTGGGTCCCTCCAGGGAGAGGAAATCTATG
SEQ ID NO:5 GCTCCCTCACCCAAGCCTCAGCTATCCGAGTTGGGTCCCTCCAGGGAGAGGAAATCTATG
SEQ ID NO:9 GCTCCCTCACCCAAGCCTCAGCTATCCGAGTTGGGTCCCTCCAGGGAGAGGAAATCTATG
SEQ ID NO:11 GCTCCCTCACCCAAGCCTCAGCTATCCGAGTTGGGTCCCTCCAGGGAGAGGAAATCTATG
SEQ ID NO:13 GCTCCCTCACCCAAGCCTCAGCTATCCGAGTTGGGTCCCTCCAGGGAGAGGAAATCTATG
SEQ ID NO:15 GCTCCCTCACCCAAGCCTCAGCTATCCGAGTTGGGTCCCTCCAGGGAGAGGAAATCTATG

SEQ ID NO:1 CCCCATTCAAGAGCCTGCTTCCAATGGTTAACCCTGACGACATTGTGTTTGGGGGATGGG
SEQ ID NO:5 CCCCATTCAAGAGCCTGCTTCCAATGGTTAACCCTGACGACATTGTGTTTGGGGGATGGG
SEQ ID NO:9 CCCCATTCAAGAGCCTGCTTCCAATGGTTAACCCTGACGACATTGTGTTTGGGGGATGGG
SEQ ID NO:11 CCCCATTCAAGAGCCTGCTTCCAATGGTTAACCCTGACGACATTGTGTTTGGGGGATGGG
SEQ ID NO:13 CCCCATTCAAGAGCCTGCTTCCAATGGTTAACCCTGACGACATTGTGTTTGGGGGATGGG
SEQ ID NO:15 CCCCATTCAAGAGCCTGCTTCCAATGGTTAACCCTGACGACATTGTGTTTGGGGGATGGG

SEQ ID NO:1 ATATCAGCAACATGAACCTGGCTGATGCCATGGCCAGGGCAAAGGTGTTTGACATCGATT
SEQ ID NO:5 ATATCAGCAACATGAACCTGGCTGATGCCATGGCCAGGGCAAAGGTGTTTGACATCGATT
SEQ ID NO:9 ATATCAGCAACATGAACCTGGCTGATGCCATGGCCAGGGCAAAGGTGTTTGACATCGATT
SEQ ID NO:11 ATATCAGCAACATGAACCTGGCTGATGCCATGGCCAGGGCAAAGGTGTTTGACATCGATT
SEQ ID NO:13 ATATCAGCAACATGAACCTGGCTGATGCCATGGCCAGGGCAAAGGTGTTTGACATCGATT
SEQ ID NO:15 ATATCAGCAACATGAACCTGGCTGATGCCATGGCCAGGGCAAAGGTGTTTGACATCGATT

SEQ ID NO:1 TGCAGAAGCAGTTGAGGCCTTACATGGAATCCATGCTTCCACTCCCCGGAATCTATGACC
SEQ ID NO:5 TGCAGAAGCAGTTGAGGCCTTACATGGAATCCATGCTTCCACTCCCCGGAATCTATGACC
SEQ ID NO:9 TGCAGAAGCAGTTGAGGCCTTACATGGAATCCATGCTTCCACTCCCCGGAATCTATGACC
SEQ ID NO:11 TGCAGAAGCAGTTGAGGCCTTACATGGAATCCATGCTTCCACTCCCCGGAATCTATGACC
SEQ ID NO:13 TGCAGAAGCAGTTGAGGCCTTACATGGAATCCATGCTTCCACTCCCCGGAATCTATGACC
SEQ ID NO:15 TGCAGAAGCAGTTGAGGCCTTACATGGAATCCATGCTTCCACTCCCCGGAATCTATGACC

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SEQ ID NO:5 CGGATTTTCATTGCTGCCAACCAAGAGGAGCGTGCCAACAACGTCATCAAGGGCACAAGC
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SEQ ID NO:11 CGGATTTTCATTGCTGCCAACCAAGAGGAGCGTGCCAACAACGTCATCAAGGGCACAAGC
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SEQ ID NO:15 CGGATTTTCATTGCTGCCAACCAAGAGGAGCGTGCCAACAACGTCATCAAGGGCACAAGC

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SEQ ID NO:11 AAGAGCAAGTTCAAGCAAATCATCAAGACATCAAGGCGTTTAAGGAAGCCACCAAAGTGG
SEQ ID NO:13 AAGAGCAAGTTCAAGCAAATCATCAAGACATCAAGGCGTTTAAGGAAGCCACCAAAGTGG
SEQ ID NO:15 AAGAGCAAGTTCAAGCAAATCATCAAGACATCAAGGCGTTTAAGGAAGCCACCAAAGTGG

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SEQ ID NO:9 ACAAGGTGGTTGTACTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTTGTGGGCC

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SEQ ID NO:11 ACAAGGTGGTTGTCTGTGGACTGCCAACACAGAGAGGTATAGCAATTTGGTTGTAGGCC
SEQ ID NO:13 ACAAGGTGGTTGTCTGTGGACTGCCAACACAGAGAGGTATAGCAATTTGGTTGTAGGCC
SEQ ID NO:15 ACAAGGTGGTTGTCTGTGGACTGCCAACACAGAGAGGTATAGCAATTTGGTTGTAGGCC
Motif II

SEQ ID NO:1 TTAATGACACCATGGAGAATCTCTGGCTGCTGTGGACAGAAATGAGGCTGAGATTTCTC
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Motif III

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Motif IV

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SEQ ID NO:11 TCAGCTATCTGACCAAGGCTCCTCTGGTTCCACCGGGTACACCAAGTGGTGAATGCATTGT
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SEQ ID NO:9 CAAAGCAGCGTGCAATGCTGGAAAACATAATGAGGGCTTGTGTTGGATTGGCCCCAGAGA
SEQ ID NO:11 CAAAGCAGCGTGCAATGCTGGAAAACATAATGAGGGCTTGTGTTGGATTGGCCCCAGAGA
SEQ ID NO:13 CAAAGCAGCGTGCAATGCTGGAAAACATAATGAGGGCTTGTGTTGGATTGGCCCCAGAGA
SEQ ID NO:15 CAAAGCAGCGTGCAATGCTGGAAAACATAATGAGGGCTTGTGTTGGATTGGCCCCAGAGA

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SEQ ID NO:5 -----
SEQ ID NO:9 -----
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SEQ ID NO:1	TGCATCAGCTTCATTAATGCTTTAGAGCGGGGCATATTCTGTTTACTAGGAACATGAATG
SEQ ID NO:5	-----
SEQ ID NO:9	-----
SEQ ID NO:11	-----
SEQ ID NO:13	-----
SEQ ID NO:15	-----
SEQ ID NO:1	AATGTAGTATAATTTTGTGT
SEQ ID NO:5	-----
SEQ ID NO:9	-----
SEQ ID NO:11	-----
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